

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions,  
and listings of claims in the application:

LISTING OF CLAIMS:

1-43. (canceled)

44.(previously presented) Mutated V1/AR1/AV1 or C1/AL1/AC1 gene sequence of a tomato infecting geminivirus wherein the mutations consist of point mutations distributed along the sequence in such a way that the continuous homology between the mutated sequence and the corresponding viral gene sequence is below or equal to 8 nucleotides, preferably below or equal to 5 nucleotides, said mutated sequence encoding for a capsid protein or for a Rep protein, respectively.

45.(previously presented) Mutated V1/AR1/AV1 gene sequence according to claim 44, encoding for a capsid protein having sequence SEQ ID No 7.

46.(previously presented) Mutated C1/AL1/AC1 gene sequence according to claim 44, wherein the mutation further comprises a truncation occurring at 3' terminal so that the mutated sequence encodes for a truncated Rep protein.

47.(previously presented) Mutated C1/AL1 /AC1 gene sequences according to claim 46, wherein the truncated Rep proteins consist of 130 aminoacids (Rep 130) to 210 aminoacids (Rep 210).

48.(previously presented) Mutated C1/AL1/AC1 gene sequence according to claim 46 encoding for Rep 210 SEQ ID No 3 or SEQ ID No 5.

49.(previously presented) Mutated C1/AL1/AC1 gene sequence encoding for Rep 130 SEQ ID No 9.

50.(previously presented) Mutated gene sequence according to claim 44 wherein the tomato infecting geminivirus is TYLCSV.

51.(previously presented) Synthetic construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

a) polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;

b) a non translated polynucleotide sequence positioned 5' of the encoding region;

c) a mutated gene sequence;

d) a sequence acting as transcription terminator, positioned 3' with respect to the mutated gene sequence.

52.(previously presented) Expression vector comprising the construct as defined according to claim 51.

53.(previously presented) Transgenic plant, tissue or plant cells thereof, comprising in their genome a mutated gene sequence according to claim 43.

54.(previously presented) Seed comprising in its genome a mutated gene sequence according to claim 43.

55.(currently amended) ~~Method~~ A method for the preparation of transgenic plants, plant tissue or cells thereof having long lasting resistance against geminiviruses, including the following steps:

a) identification or selection of a ~~viral gene~~ geminivirus gene-derived sequence encoding an ~~amino acid~~ amino acid sequence able to confer resistance against geminiviruses;

b) mutagenesis of the ~~viral gene sequence~~ geminivirus gene-derived sequence, wherein the mutations consist of point mutations distributed along the geminivirus gene-derived sequence so that continuous homology between the mutated sequences and the corresponding viral gene sequence is less than or equal to 8 nucleotides or less than or equal to 5 nucleotides ~~so as to make it an ineffective target of the post-~~

~~transcriptional gene silencing induced by the infecting  
geminivirus;~~

c) insertion of the geminivirus gene sequence mutated in the step b) in the plant, plant tissue or cell thereof, using a construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

i) a polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;

ii) a non translated polynucleotide sequence positioned 5' of the encoding region;

iii) a polynucleotide sequence encoding a geminivirus-derived ~~amino acid~~ amino acid sequence, properly mutagenised according to step (b) to be an ineffective target of the post-transcriptional gene silencing induced by the infecting geminivirus;

iv) a sequence acting as transcription terminator positioned 3' with respect to said polynucleotide sequence.

56-57. (cancelled)

58. (currently amended) ~~Method~~ The method according to claim 55, wherein the geminiviruses are selected from the ~~group consisting of species of Mastrevirus, Curtovirus, belonging to the Begomovirus genus and Topocuvirus and~~ isolates thereof.

59. (currently amended) ~~Method~~ The method according to claim 58, wherein the Begomoviruses species are ~~selected from the group consisting of TYLCCNV, TYLCGV, TYLCMaIV, is TYLCSV, TYLCTHV, TYLCV, ACMV, BGMV, CaLCuV, ToCMoV, TCMV, ToGMoV, ToMHV, ToMoTV, ToMoV, ToRMV, ToSLCV, ToSRV, Cotton leaf curl (CLCrV, CLCuAV, CLCuGV, CLCuKV, CLCuMV, CLCuRV), East African cassava mosaic (EACMCV, EACMMV, EACMV, EACMZV), Potato yellow mosaic (PYMPV, PYMTV, PYMV), Squash leaf curl (SLCCNV, SLCV, SLCYV), Sweet potato leaf curl (SPLCGV, SPLCV), Tobacco leaf curl (TbLCJv, TbLCKoV, TbLCYNV, TbLCZV), Tomato leaf curl (ToLCBV, ToLCBDV, ToLCGV, ToLCKV, ToLCLV, ToLCMV, ToLCNDV, ToLCSLV, ToLCTWV, ToLCVV, ToLCV) and isolates thereof.~~

60. (cancelled)

61. (currently amended) ~~Method~~ The method according to claim 55, wherein the gene sequence is selected from the group consisting of C1/AL1/AC1, C2/AL2/AC2, C3/AL3/AC3, C4/AL4/AC4, V1/AR1/AV 1, V2/AR2/AV2, BC1/BL1 and BV1/BR1, ~~belonging to the geminiviruses~~ belonging to TYLCSV.

62. (cancelled)

63.(currently amended) ~~Method~~The method according to claim ~~62~~61, wherein the ~~amino acid~~amino acid sequence is a truncated protein with respect to the viral wild-type protein.

64.(currently amended) ~~Method~~The method according to claim 63 wherein the viral gene sequences made ineffective targets of the virus-induced posttranscriptional gene silencing ~~are the~~is SEQ ID No 8, ~~SEQ ID No 2 and SEQ ID No 4.~~

65.(currently amended) ~~Method~~The method according to claim 64, wherein the truncated ~~proteins are~~protein is Rep-130 (SEQ ID No 9) ~~or Rep 210 (SEQ ID No 3 and 5).~~

66-67.(cancelled)

68.(currently amended) ~~Method~~The method according to claim 55, wherein the plants, tissues or cells thereof belong to the group consisting of tomato, pepper, tobacco, squash, manioc, sweet potato, cotton, melon, potato, soybean, corn, wheat, sugar cane, bean, beet.